

Exhibit IX

7.971	CCCTCCGCTCCATTCGCCCTTACCGCTCTGGACAGATGCGAGGGCCCTGTCAAGGCC 8030
8.041	CCAGTGCGCTCGTICGTTCCGCCAGACTGCCAACGAGATTCCTGGAAACCCA 8100
8.031	CCAGTGCGCTCGTCCGCTCCCAAGACTGCCAACGAGATTCCTGGAAACCCA 8090
8.1101	GTCAGGCCAGGTGGGGACAAGGGCAGGGCTGGCTGGCCCTGGGGAAAGGGATCTCCGA 8160
8.091	GTCAGGCCAGGTGGGGACAAGGGCAGGGCTGGCTGGCCCTGGGGAAACGGATCTCCGA 8150
8.161	GGACTGAGACTGTTTACACATCGTTCGGAGCGTGGAGAAGGGAGATGTA 8220
8.151	GGACTGAGACTGTTTACACATCGTTCGGAGCGTGGAGAAGGGAGATGTA 8210
8.221	AATGATGCTGGTACAGGTTAACAGGTTATTTGATACTCTCATGAAATTCAAGATGTT 8280
8.211	AATGATGCTGGTACAGGTTAACAGGTTATTTGATACTCTCAAGTTAACAGATGTT 8270
8.281	TTACGCAAGGAAGGACTTACCCAGTATTACTGCTGCTGCTTGTATCTGCTTACCG 8340
8.271	TTACGCAAGGAAGGACTTACCCAGTATTACTGCTGCTGCTTGTATCTGCTTACCG 8330
8.341	TTCAGAGGGCTGTCAGGCCAGTCTCGTGAACCCATCACTCGAGAACCAAGGGGC 8400
8.331	TTCAGAGGGCTGTCAGGCCAGTCTCGTGAACCCATCACTCGAGAACCAAGGGGC 8390
84.01	GGGAACCTGCTCGTCAAGGCCGAGCTGCTGCTCCCTCCCTCCCTCCCTCCCTCC 8460
83.91	GGGAACCTGCTCGTCAAGGCCGAGCTGCTGCTCCCTCCCTCCCTCCCTCCCTCC 8450
84.61	TTCGATGCGTATTCTGTCGGCCCATTTGCGCAGGGTGGTATTCTGTCATTACCA 8520
84.51	TTCGATGCGTATTCTGTCGGCCCATTTGCGCAGGGTGGTATTCTGTCATTACCA 8510
85.21	CGGCTGTCPAAATTAAAAGGAATTATACTCCAAAAA.....AAAAA 8571
85.11	CGGCTGTCPAAATTAAAAGGAATTATACTCCAAAAA.....AAAAA 8561

SULT 2				
125672	AF125672	8686 bp	mRNA	linear
CDS	Homo sapiens silencing mediator of retinoic acid and thyrroid hormone receptor extended isoform (SMRTRE) mRNA, complete cds.		PRI 04-APR-1999	
DEFINITION				
EXPRESSION	AF125672	1	GT-4559297	

NAME	<i>Homo sapiens</i>
SOURCE	<i>Homo sapiens</i>
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE	1. (bases 1 to 8686)
AUTHORS	Park, E.J., Schrein, D.
TITLE	Silence, a silencing mechanism receptors-extended is receptor corepressor
JOURNAL	Proc. Natl. Acad. Sci.
PUBLMED	10097068
AUTHORS	Chen, J.D.
TITLE	Direct Submission
JOURNAL	Submitted 03-FEB-1994 University of Massach-
	Worcester, MA 01555, Location/Qua-
FEATURES	1. *8686
source	/organism="
	/mol type="
	/db_xref="
	1. *8686
	/gene="SMRT1"

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Query Match % Score DB % Length

Best Local Similarity 98.6%; Pred. No. 0; Mismatches 1; Indels 34; Gaps 4; Matches 8472; Conservative

156	CATGTCGGCTCCACAGCCCTCTGGCAAGAGTGGGGGCACTGAGCCGGCTACCC	215
61	GCCCCAAGCCCTTTCTAACCCAGTGCAATGCCCGAACGGCACAGCAGCTGGCTCT	120
216	GCCCCAAGCCCTTTCTAACCCAGTGCAATGCCCGAACGGCACAGCAGCTGGCTCT	275
121	GGAGTACAGGACCACTCCCGCGCACTATGCCCTCCACCTGTCCGGGTCCATATCCA	180
276	GGAGTACAGGACCACTCCCGCGCACTATGCCCTCCACCTGTCCGGGTCCATATCCA	335
181	GCCCCAGCGCGAGGCCCTCCGTGCTCTGAGTTCAGGCCGAATGAAACGGTCCCA	240

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2401	TGAGCCACCGAACCCCTAACGCCAACCCCATGCCCTCTGCACCTCC	2460	Db	GCCTGCCATGCCAACCCCCATGCCCTCTGCACCTCC	3582
2502	TGAGCCACCTAACGCCAACCCATTGCCCTCACCTCT	2561	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3517
2461	TGCTGTCCCAGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGGG	2520	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3642
2562	TGCTGTCCCAGAAGGAGAGAGAGAGAGAGAGAGAGAGAGGG	2621	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3577
2521	GGAGGAAGCAGAACGCCCGGGCTGAGAGCTGAGAGAGAGAGAG	2580	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3701
2622	GGAGGAAGCAGAACGCCCGGGCTGAGAGCTGAGAGAGAGAG	2681	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3636
2581	GCCCCATCAAGGCCAGTGGCAAGGAGCTGAGAGAGAGAGAG	2640	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3761
2682	GCCCCATCAAGGCCAGTGGCAAGGAGCTGAGAGAGAGAG	2741	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3756
2641	GGAGGGCTAACGGCAAGGCCAGGAGAGAGAGAGAGAGAG	2700	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3881
2802	CGGAAAGGCCACACAAAGCTCAAGTCC	2861	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3822
2742	GAGGGGGCTGAGGCCAGGGCTGAGGCCAGGGAGAGAGAG	2801	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3816
2701	CGGCAAGCACCACCTCCAAAGGCTGAGCTGGGGCCCTAC	2760	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3941
2862	CTGCAATGCGAGCAGGCTGGATGGCTGGATGGCTGGCTG	2820	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3882
2761	CTGCAATGCGAGCAGGCTGGATGGCTGGATGGCTGGCTG	2921	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3876
2862	CTGCAATGCGAGCAGGCTGGATGGCTGGATGGCTGGCTG	2880	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3881
2821	AAGGCCAACGCTTCAACCAAGCTGGCTGGCTGGCTGG	2981	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3942
2952	AAGGCCAACGCTTCAACCAAGCTGGCTGGCTGGCTGG	2981	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3936
2881	AATGGACCTTGAAAGCAGGAAAGGAGGGCTGGCTGG	2940	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	3877
2982	AATGGACCTTGAAAGCAGGAAAGGAGGGCTGGCTGG	3041	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4061
2941	AGTCATAGGCCCTCCAGGAGCTCCAAACAAAGGAGCTCC	3000	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4001
3042	AGTCATAGGCCCTCCAGGAGCTCCAAACAAAGGAGCTCC	3101	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4116
3001	GCCAGCGAAAACCTGCAAGCGGAAGCGAACGCCCG	3060	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4121
3102	GCCAGCGAAAACCTGCAAGCGGAAGCGAACGCCCG	3161	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4182
3061	GGCGAGAGGAGGAGGCCGACCCCGCGCAAGGGAG	3100	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4117
3162	GGCGAGAGGAGGCCGACCCCGCGCAAGGGAG	3221	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4236
3101	---CCCTTGCGAGGCCGAGCCAGAACGCCCTGGCTGG	3156	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4302
3222	CCCAAGCTTCCAGGGAGGCCCTGGCTGGACTCCGG	3281	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4237
3157	CCTGGCCCTTCCAGGGAGGCCCTGGCTGGACTCCGG	3216	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4362
3282	CCTGGCCCTTCCAGGGAGGCCCTGGCTGGACTCCGG	3341	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4297
3217	CTCAAGCTTCCATGCCCTGGCTGGCTCCATGCC	3276	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4417
3342	CTCAAGCTTCCATGCCCTGGCTGGCTCCATGCC	3401	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4357
3277	CGGGCCCTGCTGGCGGCCAACCCACCATCTCC	3336	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4482
3402	CGGGCCCTGCTGGCGGCCAACCCACCATCTCC	3461	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4417
3337	CAAGCAACCCAGGCTCTCGAGGCAATAAGGGCCATCTCC	3396	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4512
3462	CAAGCAACCCAGGCTCTCGAGGCAATAAGGGCCATCTCC	3521	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4477
3397	GCTCACCTCCGTACTCGAGGCTGCAAGGCCACCCCTT	3456	Db	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4661
3522	GCTCACCTCCGTACTCGAGGCTGCAAGGCCACCCCTT	3516	Qy	GCCCCACGGGGCAGACTGGCCACCGAGCTGGGGG	4596

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